

Query= SEQ ID NO:3
 (1047 letters)

Sequences producing significant alignments: Score E
 (bits) Value

AC008121.33.67777.200926 546 e-153

>AC008121.33.67777.200926
 Length = 133150

Score = 546 bits (275), Expect = e-153
 Identities = 275/275 (100%)
 Strand = Plus / Plus

Query: 382 agcgatcctttaatgtggacagctgtgattggaactaataatatacatggacgctatcct 441
 |||
 Sbjct: 51038 agcgatcctttaatgtggacagctgtgattggaactaataatatacatggacgctatcct 51097

Query: 442 cataccaagaagataaaaaattaaagcaatcattattcatccaaacttcattttggaatct 501
 |||
 Sbjct: 51098 cataccaagaagataaaaaattaaagcaatcattattcatccaaacttcattttggaatct 51157

Query: 502 tatgtaaatagatattgcactttttcacttaaaaaaagcagtgaggtataatgactatatt 561
 |||
 Sbjct: 51158 tatgtaaatagatattgcactttttcacttaaaaaaagcagtgaggtataatgactatatt 51217

Query: 562 cagcctatttgcctaccttttgatgttttcctgacggaaacacaaagtgtttt 621
 |||
 Sbjct: 51218 cagcctatttgcctaccttttgatgttttcctgacggaaacacaaagtgtttt 51277

Query: 622 ataagtggctggggaagaacaaaagaagaaggtaa 656
 |||
 Sbjct: 51278 ataagtggctggggaagaacaaaagaagaaggtaa 51312

Score = 502 bits (253), Expect = e-139
 Identities = 253/253 (100%)
 Strand = Plus / Plus

Query: 795 ggggtgacagtgaggggaccattaatgtgctacttaccagaatataaaagatTTTTTgtaat 854

Query: 79648 ggggaattaccagttacggacatggctgtggcgaagaggTTTTTcctgggtgtctatattgg 79707

Query: 915 gccatccttctacccaaaagtggctgacagagcatttcttccatgcaagcactcaaggcat 974
|||||
Sbjct: 79708 gccatccttctacccaaaagtggctgacagagcatttcttccatgcaagcactcaaggcat 79767

Query: 975 acttactataaatattttacgtggccagatcctcatagctttatgttttgtcatcttact 1034
|||||
Sbjct: 79768 acttactataaatattttacgtggccagatcctcatagctttatgttttgtcatcttact 79827

Query: 1035 agcaacaacataa 1047
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Sbjct: 79828 agcaacaacataa 79840

Score = 387 bits (195), Expect = e-105
Identities = 196/197 (99%)
Strand = Plus / Plus

Query: 187 gattgtggaacagcaccgcttaaggatgtgttgcaagggtctcggtattatagggggcacc 246
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Sbjct: 36091 gattgtggaacagcaccgcttaaggatgtgttgcaagggtctcggtattatagggggcacc 36150

Query: 247 gaagcacaagctggcgcatggccgtgggtggtgagcctgcagattaaatatggccgtgtt 306
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Sbjct: 36151 gaagcacaagctggcgcatggccgtgggtggtgagcctgcagattaaatatggccgtgtt 36210

Query: 307 cttgttcatgtatgtgggggaaccctagtgtgagagagaggtgggtcctcacagctgccac 366
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Sbjct: 36211 cttgttcatgtatgtgggggaaccctagtgtgagagagaggtgggtcctcacagctgccac 36270

Query: 367 tgcactaaagacrctag 383
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Sbjct: 36271 tgcactaaagacactag 36287

Score = 363 bits (183), Expect = 9e-98
Identities = 185/187 (98%)
Strand = Plus / Plus

Query: 1 atgcggctggggctcctgagcgtggcgytggtgtttgtggggagctctcacttayactca 60
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Query: 35275 gaccaactactcgccctctggaaggcacaggtcggccctcgccggaaccggcggtagt 35334
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Query: 121 tcccagcaggctgaggccgtccgcaagaggctccggcggcggagggagggaggggagggcgcat 180
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Query: 181 gcaaagg 187
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Sbjct: 35395 gcaaagg 35401

Score = 290 bits (146), Expect = 1e-75
Identities = 146/146 (100%)
Strand = Plus / Plus

Query: 651 aggtaacgctacaaatattttacaagatgcagaagtgcattatatttctcgagagatgtg 710
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Query: 711 taattctgagaggagttatgggggaataattcctaacacttcattttgtgcaggtgatga 770
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Sbjct: 77631 taattctgagaggagttatgggggaataattcctaacacttcattttgtgcaggtgatga 77690

Query: 771 agatggagcttttgatacttgcaggg 796
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Sbjct: 77691 agatggagcttttgatacttgcaggg 77716



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Details

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LOCUS AC008121 105989 bp DNA linear PRI 01-MAR-2003
DEFINITION Homo sapiens 12 BAC RP11-407N8 (Roswell Park Cancer Institute Human BAC Library) complete sequence.
ACCESSION AC008121
VERSION AC008121.43 GI:28626577
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 105989)
AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chiu,D., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Emerling,S., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Han,J., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B., Homsí,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Ioshikhes,I., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lee,E., Lewis,L.C., Lewis,D., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P., Marondel,I., Martin,R., Martindale,A., Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Merscher,S.,

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Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y.,
Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savory, G.,
Schepers, J., Shattuck, H., Shaw, D., Shih, L., Shih, L.,
Shin, K., Smith, T., Soane, J., Spence, J., Stachurski, P.,
Stallins, A., Stone, A., Sullivan, A., Swartz, A., Tammara, F., Taylor,

>XM_171629 ACCESSION:XM_171629 NID: gi 22062231 ref XM_171629.1 Homo
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 precursor (LOC257238), mRNA
 Length = 1295

Identities = 141/153 (92%), Positives = 141/153 (92%)
 Frame = +3

Query: 62 CGTAPLKDVLQGSRIIGGTEAQAGAWPWVSLQIKYGRVLVHVCGGTLVRERWVLTAAHC 121
 CGTAPLKDVLQGSRIIGGTEAQAGAWPWVSLQIKYGRVLVHVCGGTLVRE
 Sbjct: 3 CGTAPLKDVLQGSRIIGGTEAQAGAWPWVSLQIKYGRVLVHVCGGTLVRE----- 155

Query: 122 TKDSDPLMWTAVIGTNNIHGRYPHTKKIKIKAIHHPNFILESVNDIALFHLKKAVRYN 181
 SDPLMWTAVIGTNNIHGRYPHTKKIKIKAIHHPNFILESVNDIALFHLKKAVRYN
 Sbjct: 156 ---SDPLMWTAVIGTNNIHGRYPHTKKIKIKAIHHPNFILESVNDIALFHLKKAVRYN 326

Query: 182 DYIQPICLPFDVQILDGNTKCFISGWGRTKEE 214
 DYIQPICLPFDVQILDGNTKCFISGWGRTKEE
 Sbjct: 327 DYIQPICLPFDVQILDGNTKCFISGWGRTKEE 427

Identities = 131/131 (100%), Positives = 131/131 (100%)
 Frame = +3

Query: 215 GNATNILQDAEVHYISREMCNSERSYGGIIPNTSFCAGDEDGAFDTCRGDSGGPLMCYLP 274
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 Sbjct: 900 GNATNILQDAEVHYISREMCNSERSYGGIIPNTSFCAGDEDGAFDTCRGDSGGPLMCYLP 1079

Query: 275 EYKRFFVMGITSYGHGCGRRGFPVYIGPSFYQKWLTEHFFHASTQGILTINILRGQILI 334
 EYKRFFVMGITSYGHGCGRRGFPVYIGPSFYQKWLTEHFFHASTQGILTINILRGQILI
 Sbjct: 1080 EYKRFFVMGITSYGHGCGRRGFPVYIGPSFYQKWLTEHFFHASTQGILTINILRGQILI 1259

Query: 335 ALCFVILLATT 345
 ALCFVILLATT
 Sbjct: 1260 ALCFVILLATT 1292

/note="Region: smart00020, Tryp_SPC, Trypsin-like serine protease; Many of these are synthesised as inactive precursor zymogens that are cleaved during limited proteolysis to generate their active forms. A few, however, are active as single chain molecules, and others are inactive due to substitutions of the catalytic triad residues"

misc_feature

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/gene="LOC257238"

/note="Region: pfam00089, trypsin, Trypsin"

misc_feature

819..1199

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/note="Region: pfam02395, IGA1, Immunoglobulin A1 protease. This family consists of immunoglobulin A1 protease proteins. The immunoglobulin A1 protease cleaves immunoglobulin IgA and is found in pathogenic bacteria such as Neisseria gonorrhoeae. Not all of the members of this family are IgA proteases (one member from E. coli cleaves human coagulation factor V, another one is a hemoglobin protease)"

misc_feature

900..1187

/gene="LOC257238"

/note="Region: smart00020, Tryp_SPC, Trypsin-like serine protease; Many of these are synthesised as inactive precursor zymogens that are cleaved during limited proteolysis to generate their active forms. A few, however, are active as single chain molecules, and others are inactive due to substitutions of the catalytic triad residues"

misc_feature

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variation

681

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121 ttgttcatgt atgtggggga accctagtga gagagagcga tcctttaatg tggacagctg
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1201 tcatctcaag catccaagg atacttacta ttttatatt acgtggccag atcctcatag
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1261 ctttatgttt tgatcatccta ctagcaacaa cataa
//

Revised: July 5, 2002.

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Dec 2 2002 13:45:47

>XM_208689 ACCESSION:XM_208689 NID: gi 30157117 ref XM_208689.3
Homo sapiens similar to adrenal secretory serine
protease precursor (LOC283471), mRNA
Length = 1457

Score = 712 bits (1819), Expect = 0.0

Identities = 344/348 (98%), Positives = 345/348 (98%), Gaps = 3/348 (0%)

Frame = +1

Query: 1 MRLGLLSVAL-FVGSSHL-SDHYSPSGRHRRLGPSPEPAASSQQAEAVRKRLRRRREGGAH 58
MRLGLLSVAL FVGSSHL SDHYSPSGRHRRLGPSPEPAASSQQAEAVRKRLRRRREGGAH
Sbjct: 40 MRLGLLSVALLFVGSSHLSDHYSPSGRHRRLGPSPEPAASSQQAEAVRKRLRRRREGGAH 219

Query: 59 AKDCGTAPLKDV LQGSRIIGGTEAQAGAWPWVSLQIKYGRVLVHVCGGTLVRERWVLTA 118
A+DCGTAPLKDV LQGSRIIGGTEAQAGAWPWVSLQIKYGRVLVHVCGGTLVRERWVLTA
Sbjct: 220 AEDCGTAPLKDV LQGSRIIGGTEAQAGAWPWVSLQIKYGRVLVHVCGGTLVRERWVLTA 399

Query: 119 AHCTKD-SDPLMWTAVIGTNNIHGRYPHTKKIKIKAI IHPNFILESYVNDIALFHLKKA 177
AHCTKD SDPLMWTAVIGTNNIHGRYPHTKKIKIKAI IHPNFILESYVNDIALFHLKKA
Sbjct: 400 AHCTKDASDPLMWTAVIGTNNIHGRYPHTKKIKIKAI IHPNFILESYVNDIALFHLKKA 579

Query: 178 VRYNDYIQPICLPFDV FQILDGNTKCFISGWGRTKEEGNATNILQDAEVHYISREMCNSE 237
VRYNDYIQPICLPFDV FQILDGNTKCFISGWGRTKEEGNATNILQDAEVHYISREMCNSE
Sbjct: 580 VRYNDYIQPICLPFDV FQILDGNTKCFISGWGRTKEEGNATNILQDAEVHYISREMCNSE 759

Query: 238 RSYGGIIPNTSFCAGDEDGAFDTCRGDSGGPLMCYLPEYKRFFVMGITSYGHGCGRRGFP 297
RSYGGIIPNTSFCAGDEDGAFDTCRGDSGGPLMCYLPEYKRFFVMGITSYGHGCGRRGFP
Sbjct: 760 RSYGGIIPNTSFCAGDEDGAFDTCRGDSGGPLMCYLPEYKRFFVMGITSYGHGCGRRGFP 939

Query: 298 GVIYIGPSFYQKWLTEHFFHASTQGILTINILRGQILIALCFVILLATT 345
GVIYIGPSFYQKWLTEHFFHASTQGILTINILRGQILIALCFVILLATT
Sbjct: 940 GVIYIGPSFYQKWLTEHFFHASTQGILTINILRGQILIALCFVILLATT 1083



Boo

Clear

Details

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Links

Documentation of NCBI's Annotation Process

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FEATURES             Location/Qualifiers
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     CDS                40..1086
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                        /codon_start=1
                        /product="similar to adrenal secretory serine protease
                        precursor"
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protease [Posttranslational modification, protein
turnover, chaperones]"
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May 2 2003 16:47:12